

**Amendments to the Claims:**

Claims 25, 29, and 33 are amended herein. This listing of claims will replace all prior versions, and listings, of claims in the application.

**Listing of Claims:**

Claims 1 -19. (canceled)

Claim 20. (previously presented) A method for analyzing a nucleic acid sample comprising:

fragmenting the nucleic acid sample using a first and a second restriction enzyme to produce fragments;

ligating a first and a second adaptor to the fragments to produce adaptor-ligated fragments, wherein the first adaptor is blocked from ligation to the fragments at the 3' end of one strand of the first adaptor, and the second adaptor is blocked from ligation to the fragments at the 5' end of one strand of the second adaptor and wherein the first adaptor ligates to the fragments cut by the first restriction enzyme and the second adaptor ligates to the fragments cut by the second restriction enzyme;

amplifying the adaptor-ligated fragments to produce amplified fragments, wherein the adaptor-ligated fragments that contain both the first adaptor and the second adaptor are enriched in the amplification product relative to the adaptor-ligated fragments that contain the first adaptor and do not contain the second adaptor, and to the adaptor-ligated fragments that contain the second adaptor and do not contain the first adaptor;

providing a nucleic acid array consisting essentially of probes designed to detect the bases present at a plurality of polymorphisms predicted to be present in the amplified fragments;

hybridizing the amplified fragments to the array; and

analyzing a hybridization pattern resulting from the hybridization.

Claim 21. (canceled)

Claim 22. (previously presented) The method of claim 20 wherein the polymorphisms are single nucleotide polymorphisms (SNPs).

Claim 23. (canceled)

Claim 24. (previously presented) The method of claim 20 wherein the polymorphisms predicted to be present in the amplified fragments are first determined by a computer system.

Claim 25. (currently amended) A method of determining the base present at a polymorphism in an individual comprising:

providing a nucleic acid sample from the individual;

fragmenting the nucleic acid sample using a first and a second restriction enzyme to produce fragments wherein the polymorphism is predicted to be on a fragment that is cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

ligating a first and a second adaptor to the fragments to produce adaptor-ligated fragments, wherein the first adaptor is blocked from ligation to the fragments at the 3' end of one strand of the first adaptor, and the second adaptor is blocked from ligation to the fragments at the 5' end of one strand of the second adaptor and wherein the first adaptor ligates to the fragments cut by the first restriction enzyme and the second adaptor ligates to the fragments cut by the second restriction enzyme; and

amplifying the adaptor-ligated fragments to produce amplified fragments, wherein the adaptor-ligated fragments that contain both the first adaptor and the second adaptor are enriched in the amplification product relative to the adaptor-ligated fragments that contain the first adaptor and do not contain the second adaptor, and to the adaptor-ligated fragments that contain the second adaptor and do not contain the first adaptor;

providing a nucleic acid array consisting essentially of probes designed to detect the bases present at a plurality of polymorphisms predicted to be present in the amplified fragments;

hybridizing the amplified fragments to the array;

generating a hybridization pattern resulting from the hybridization; and

determining the base present at the polymorphism in the individual based upon an analysis of the hybridization pattern.

Claim 26. (previously presented) The method of claim 25 wherein the polymorphism is a single nucleotide polymorphism (SNP).

Claim 27. (previously presented) The method of claim 26 wherein the SNP is associated with a disease.

Claim 28. (previously presented) The method of claim 26 wherein the SNP is associated with the efficacy of a drug.

Claim 29. (currently amended) A method of determining the base present at a single nucleotide polymorphism in a population of individuals comprising:

providing a first nucleic acid sample from each of the individuals;

providing a second nucleic acid sample by:

fragmenting the first nucleic acid sample using a first and a second restriction enzyme to produce fragments wherein the polymorphism is predicted to be on a fragment that is cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

ligating a first and a second adaptor to the fragments to produce adaptor-ligated fragments, wherein the first adaptor is blocked from ligation to the fragments at the 3' end of one strand of the first adaptor, and the second adaptor is blocked from ligation to the fragments at the 5' end of one strand of the second adaptor and wherein the first adaptor ligates to the fragments cut by the first restriction enzyme and the second adaptor ligates to the fragments cut by the second restriction enzyme; and

amplifying the adaptor-ligated fragments to produce amplified fragments, wherein the adaptor-ligated fragments that contain both the first adaptor and the second adaptor are enriched in the amplification product relative to the adaptor-ligated fragments that contain the first adaptor and do not contain the second adaptor, and to the adaptor-ligated fragments that contain the second adaptor and do not contain the first adaptor;

providing a nucleic acid array consisting essentially of probes designed to detect the bases present at a plurality of polymorphisms predicted to be present in the amplified fragments;

hybridizing each of the second nucleic acid samples to one of the plurality of identical arrays;  
generating a plurality of hybridization patterns resulting from the hybridizations; and  
analyzing the hybridization patterns to determine the bases present at the polymorphism in the population of individuals.

Claim 30. (previously presented) The method of claim 29 wherein the polymorphism is a single nucleotide polymorphism (SNP).

Claim 31. (previously presented) The method of claim 30 wherein the SNP is associated with a disease.

Claim 32. (previously presented) The method of claim 30 wherein the SNP is associated with the efficacy of a drug.

Claim 33. (currently amended) A method for genotyping an individual comprising:  
providing a first nucleic sample from the individual;  
providing a second nucleic acid sample by:  
fragmenting the first nucleic acid sample using a first and a second restriction enzyme to produce fragments wherein a collection of polymorphisms is predicted to be present in the fragments cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;  
ligating a first and a second adaptor to the fragments to produce adaptor-ligated fragments, wherein the first adaptor is blocked from ligation to the fragments at the 3' end of one strand of the first adaptor, and the second adaptor is blocked from ligation to the fragments at the 5' end of one strand of the second adaptor and wherein the first adaptor ligates to the fragments cut by the first restriction enzyme and the second adapter ligates to the fragments cut by the second restriction enzyme; and  
amplifying the adaptor-ligated fragments to produce amplified fragments, wherein the adaptor-ligated fragments that contain both the first adaptor and the second adaptor are enriched in the amplification product relative to the adaptor-ligated fragments that contain the first adaptor

and do not contain the second adaptor, and to the adaptor-ligated fragments that contain the second adaptor and do not contain the first adaptor;

providing a nucleic acid array consisting essentially of probes designed to detect the bases present at a plurality of polymorphisms predicted to be present in the amplified fragments;  
generating a hybridization pattern resulting from the hybridizations; and  
determining the bases present at one or more polymorphisms present in the collection of polymorphisms.

Claim 34. (canceled)

Claim 35. (previously presented) The method of claim 20 wherein the adaptor-ligated fragments that contain both the first adaptor and the second adaptor comprise at least 0.01% of the nucleic acid sample.

Claim 36. (previously presented) The method of claim 20 wherein the adaptor-ligated fragments that contain both the first adaptor and the second adaptor comprise at least 0.05% of the nucleic acid sample.

Claim 37. (previously presented) The method of claim 20 wherein the adaptor-ligated fragments that contain both the first adaptor and the second adaptor comprise at least 3% of the nucleic acid sample.

Claim 38. (previously presented) The method of claim 20 wherein the adaptor-ligated fragments that contain both the first adaptor and the second adaptor comprise at least 12% of the nucleic acid sample.

Claim 39. (previously presented) The method of claim 20 wherein the adaptor-ligated fragments that contain both the first adaptor and the second adaptor comprise at least 30% of the nucleic acid sample.

Claim 40. (previously presented) The method of claim 20 wherein the nucleic acid sample is genomic DNA, DNA, or double stranded cDNA derived from RNA, total RNA or mRNA.

Claim 41. (canceled)

Claim 42. (previously presented) The method of claim 20 wherein ligation is blocked by introducing a gap of at least one nucleotide between one strand of the adaptor and one strand of the fragment.

Claim 43. (previously presented) The method of claim 20 wherein ligation of the second adaptor is blocked by the absence of a phosphate at the 5' end of an adaptor strand of the second adaptor.

Claim 44. (previously presented) The method of claim 20 wherein ligation is blocked by the presence of a modified nucleotide at the 5' or 3' end of an adaptor strand.

Claim 45. (previously presented) The method of claim 20 wherein ligation is blocked by a terminal modification in one strand of an adaptor.

Claim 46. (previously presented) The method of claim 20 wherein ligation of the second adaptor is blocked at the 5' end of one strand of the second adaptor and ligation of the first adaptor is blocked at the 3' end of one strand of the first adaptor.

Claim 47. (previously presented) The method of claim 20 wherein ligation is blocked at the 5' end of both strands of the second adaptor and at the 3' end of both strands of the first adaptor.